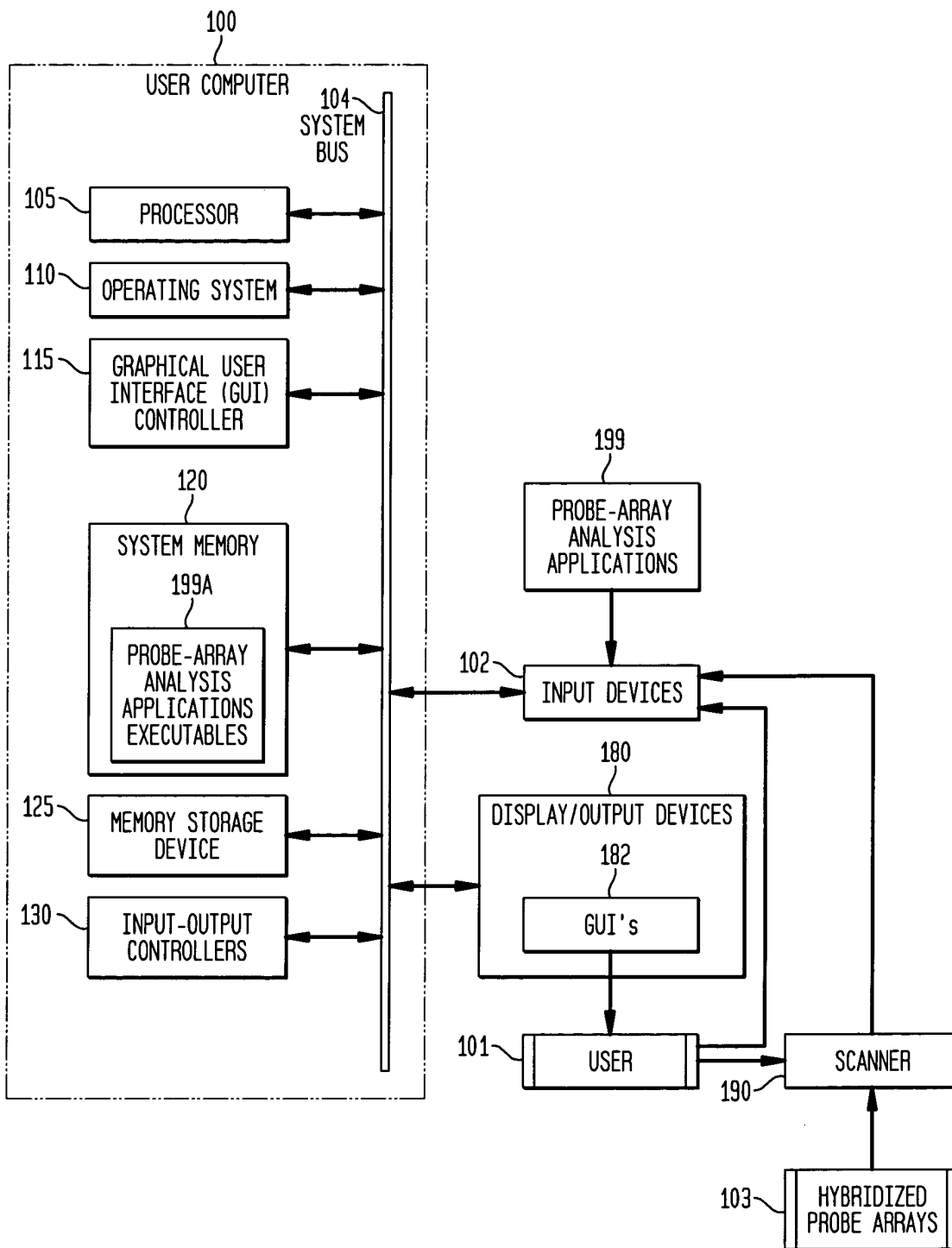


FIG. 1



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FIG. 2

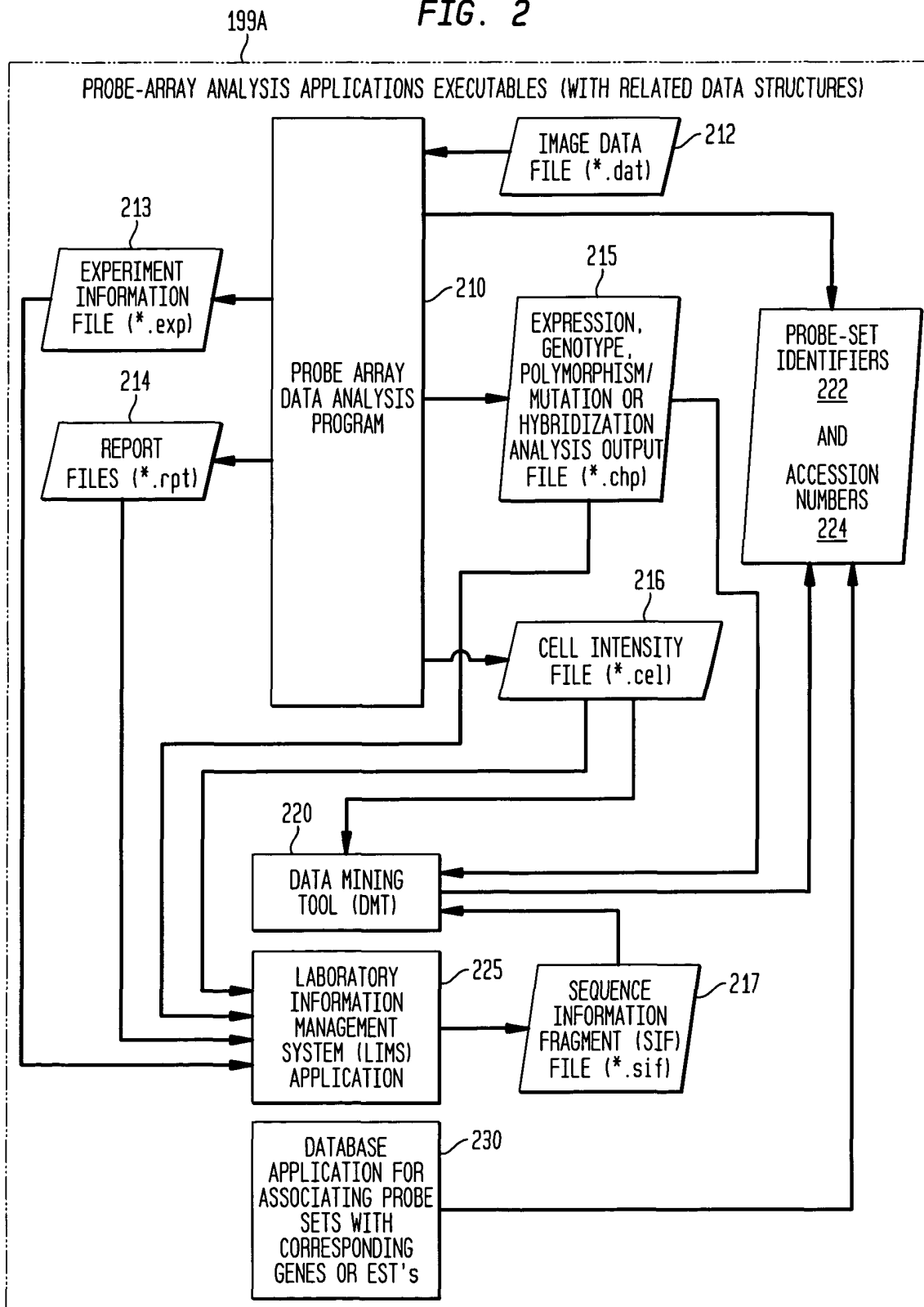
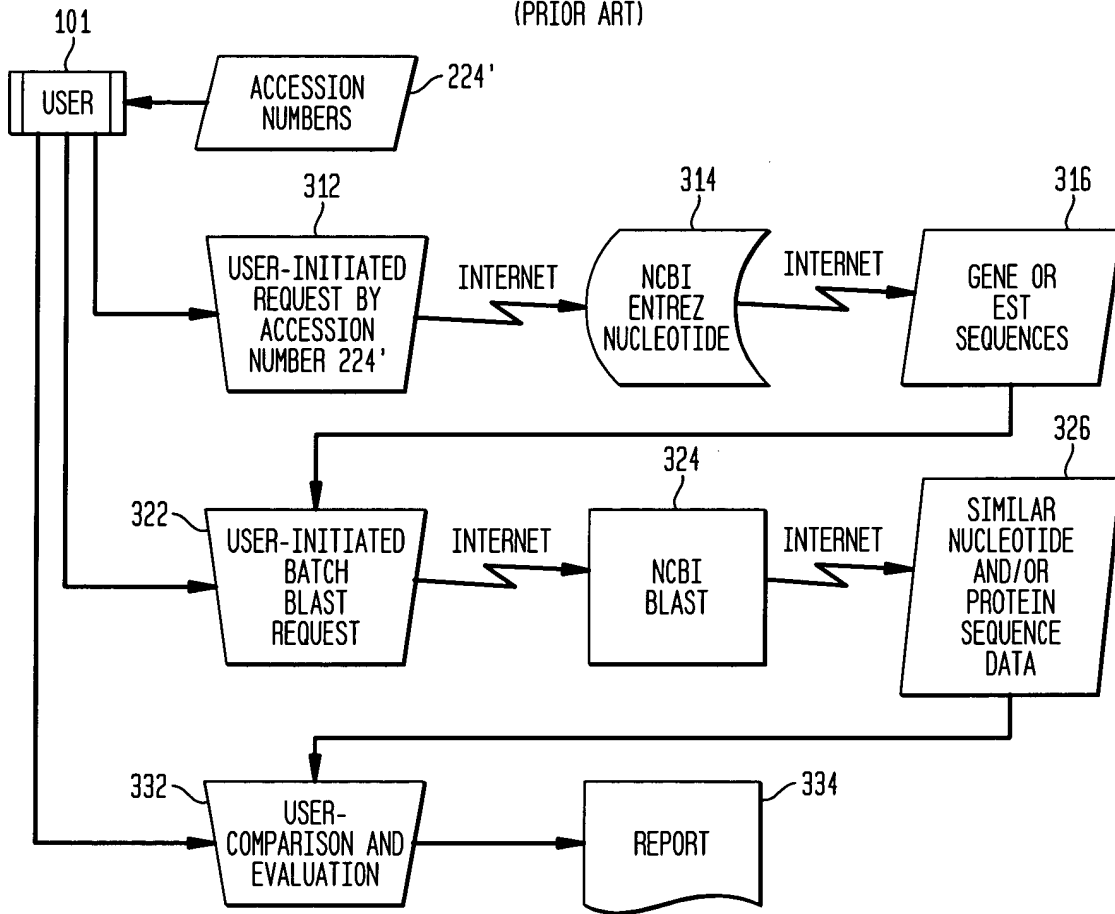
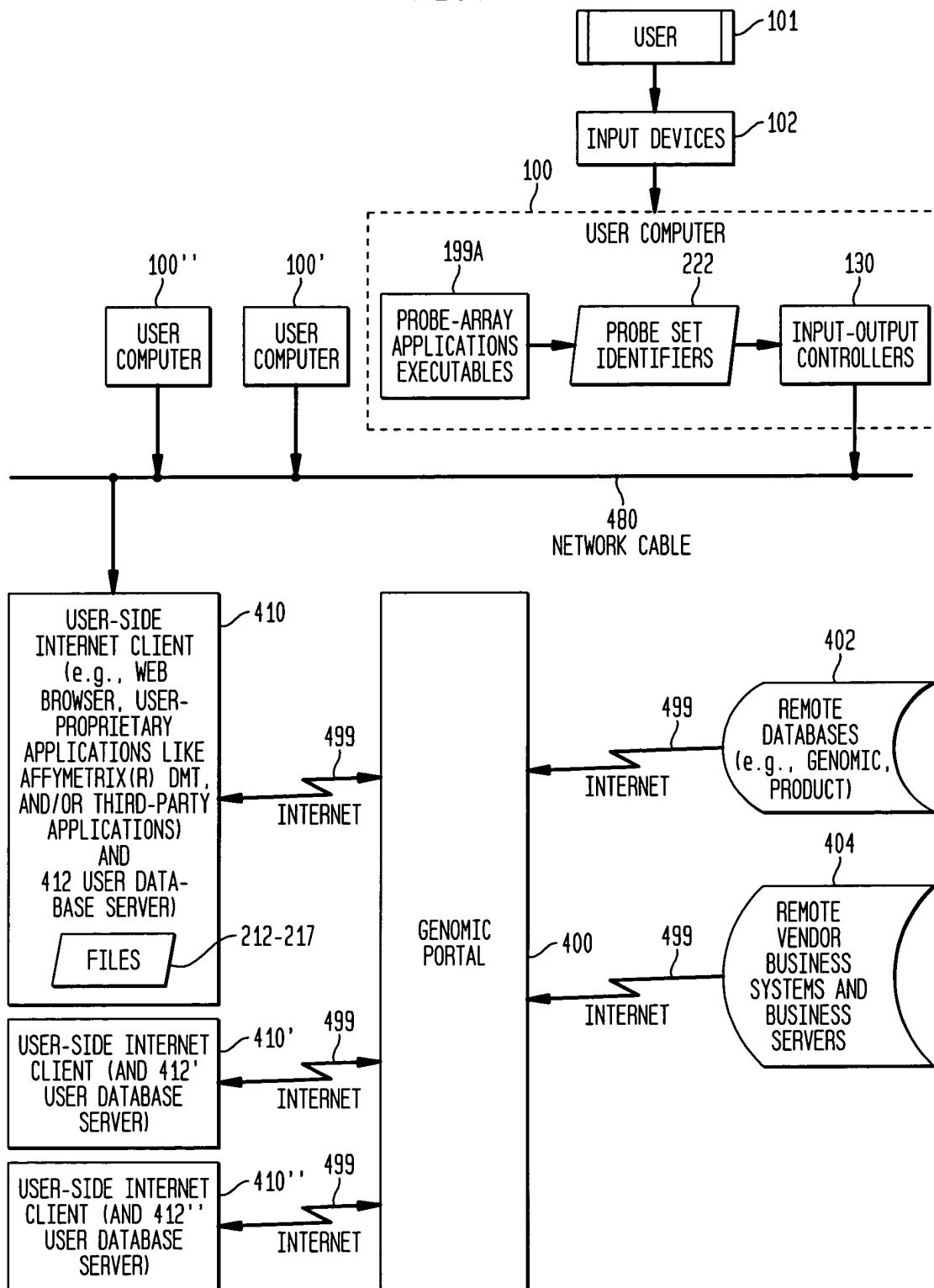


FIG. 3
(PRIOR ART)



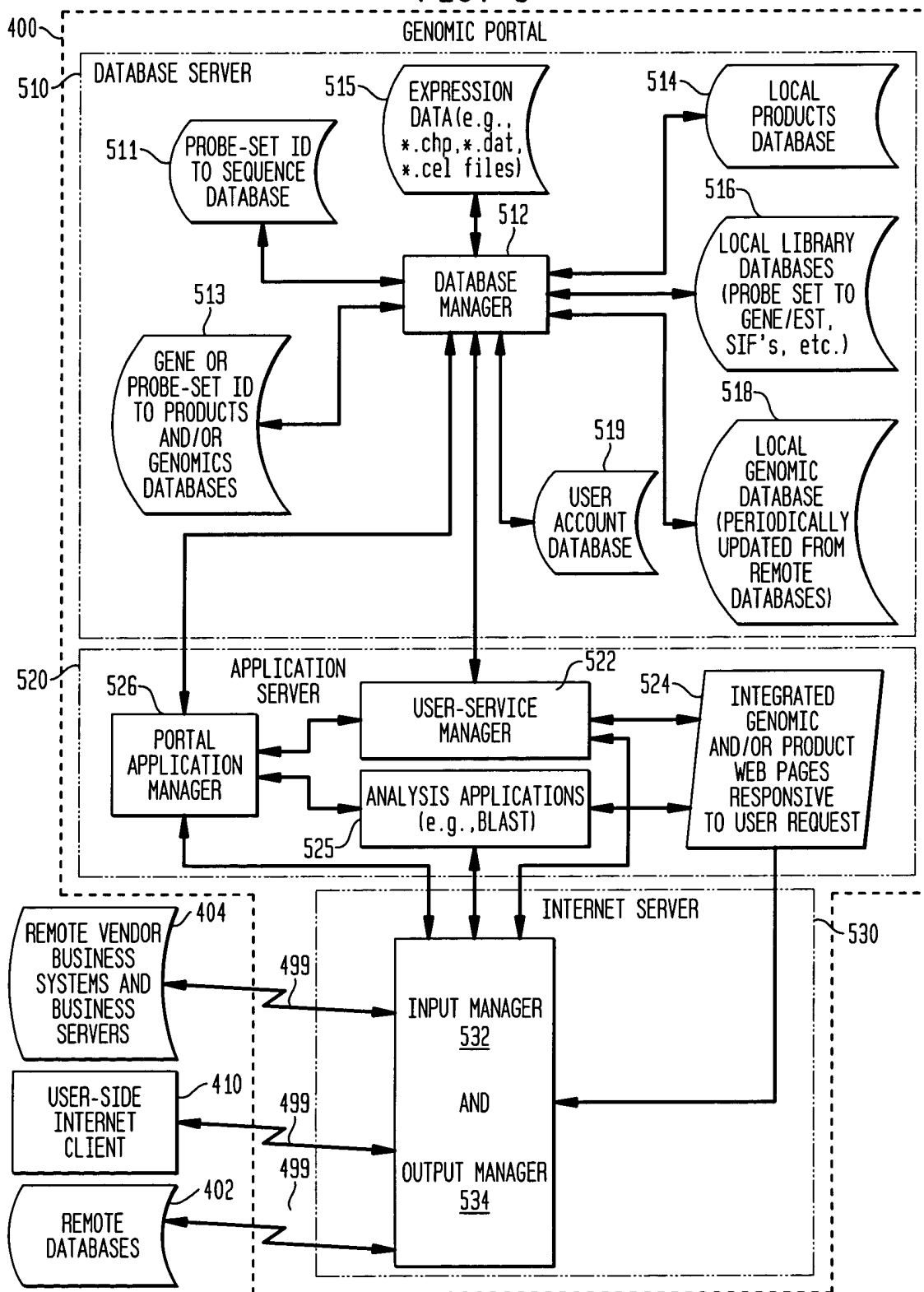
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FIG. 4

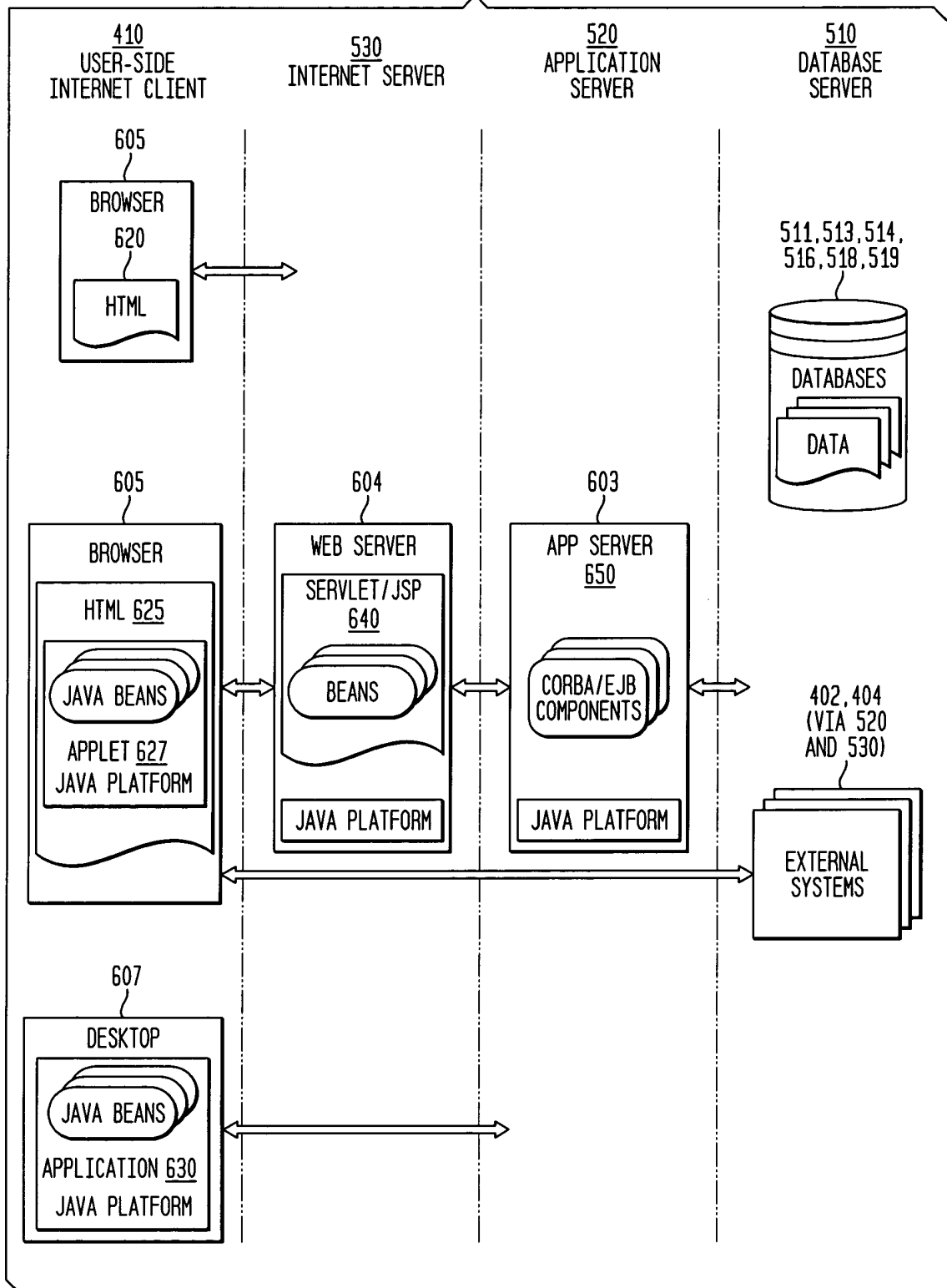


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FIG. 5

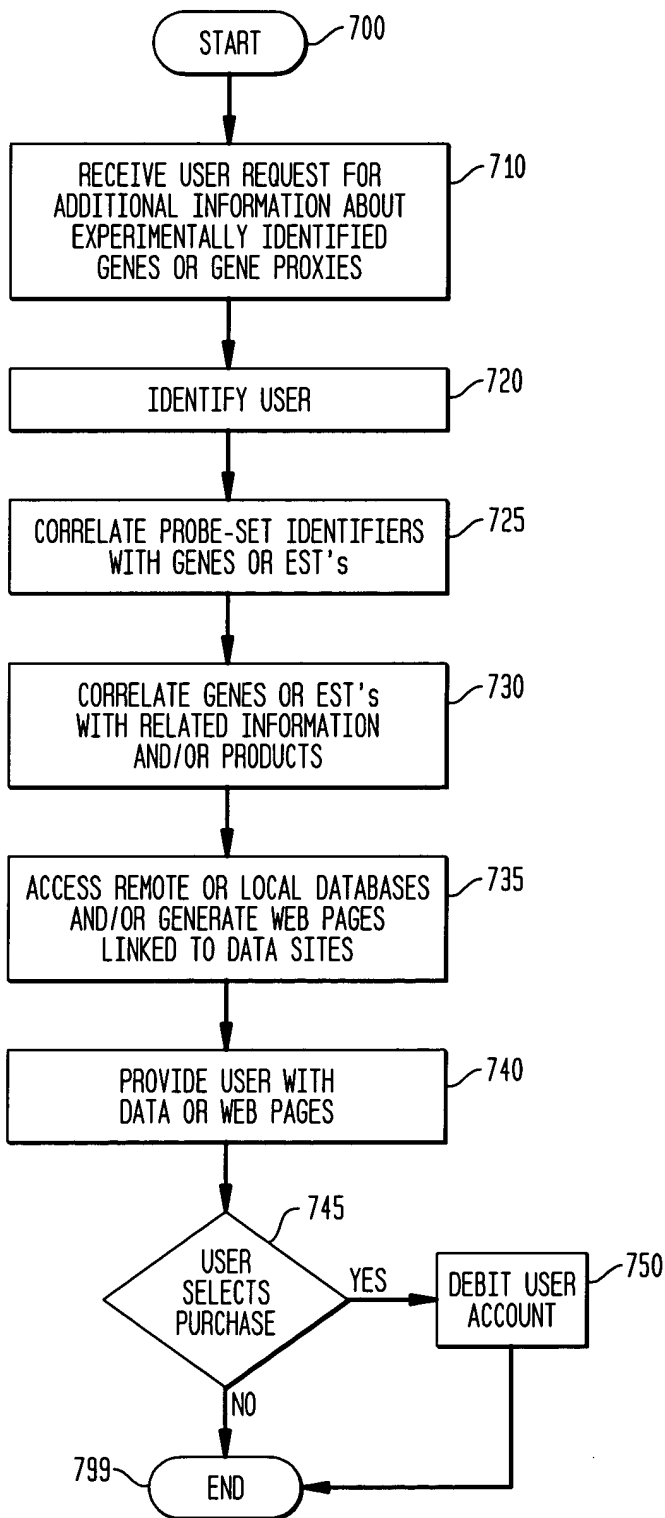


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FIG. 6



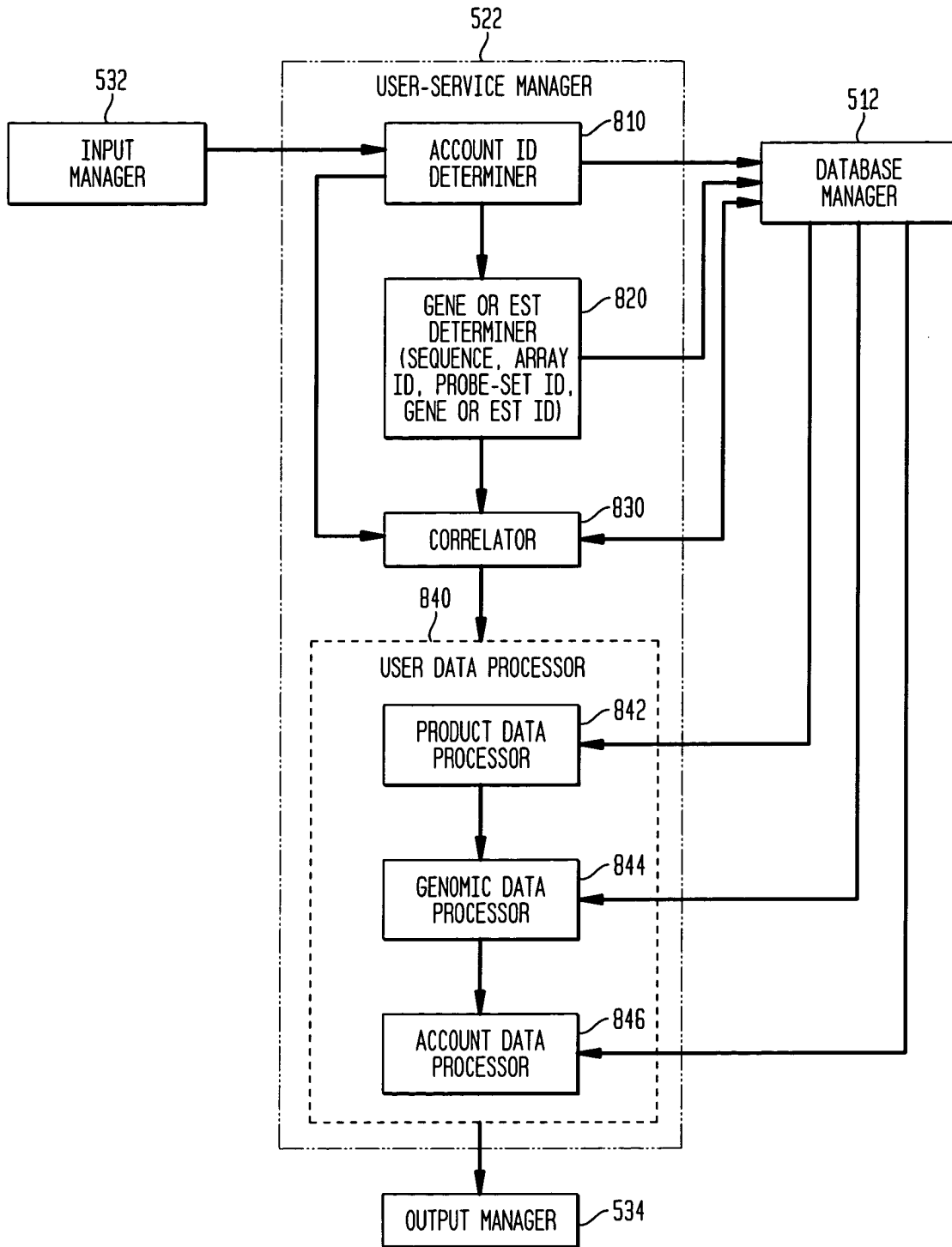


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FIG. 7



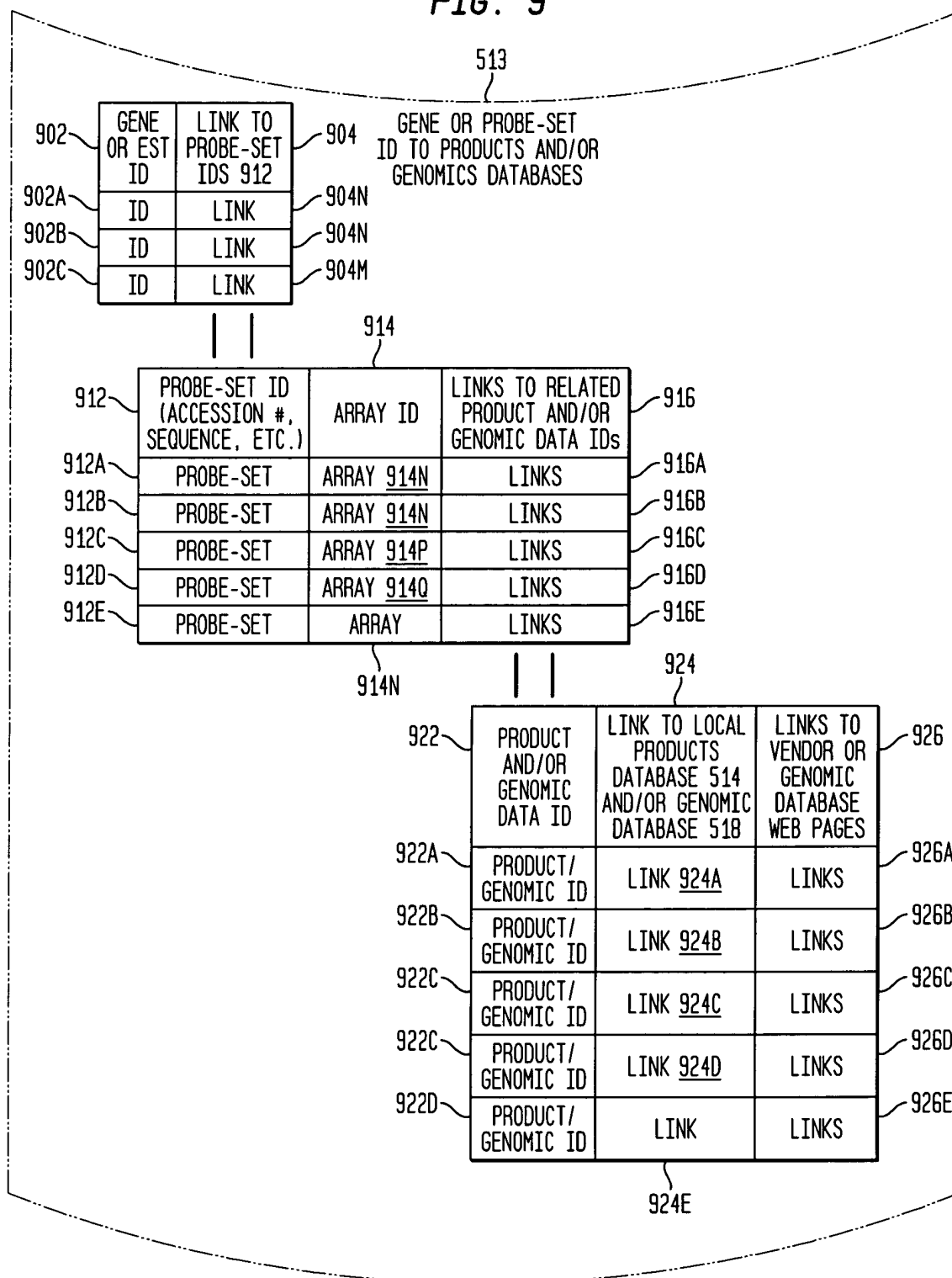
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FIG. 8

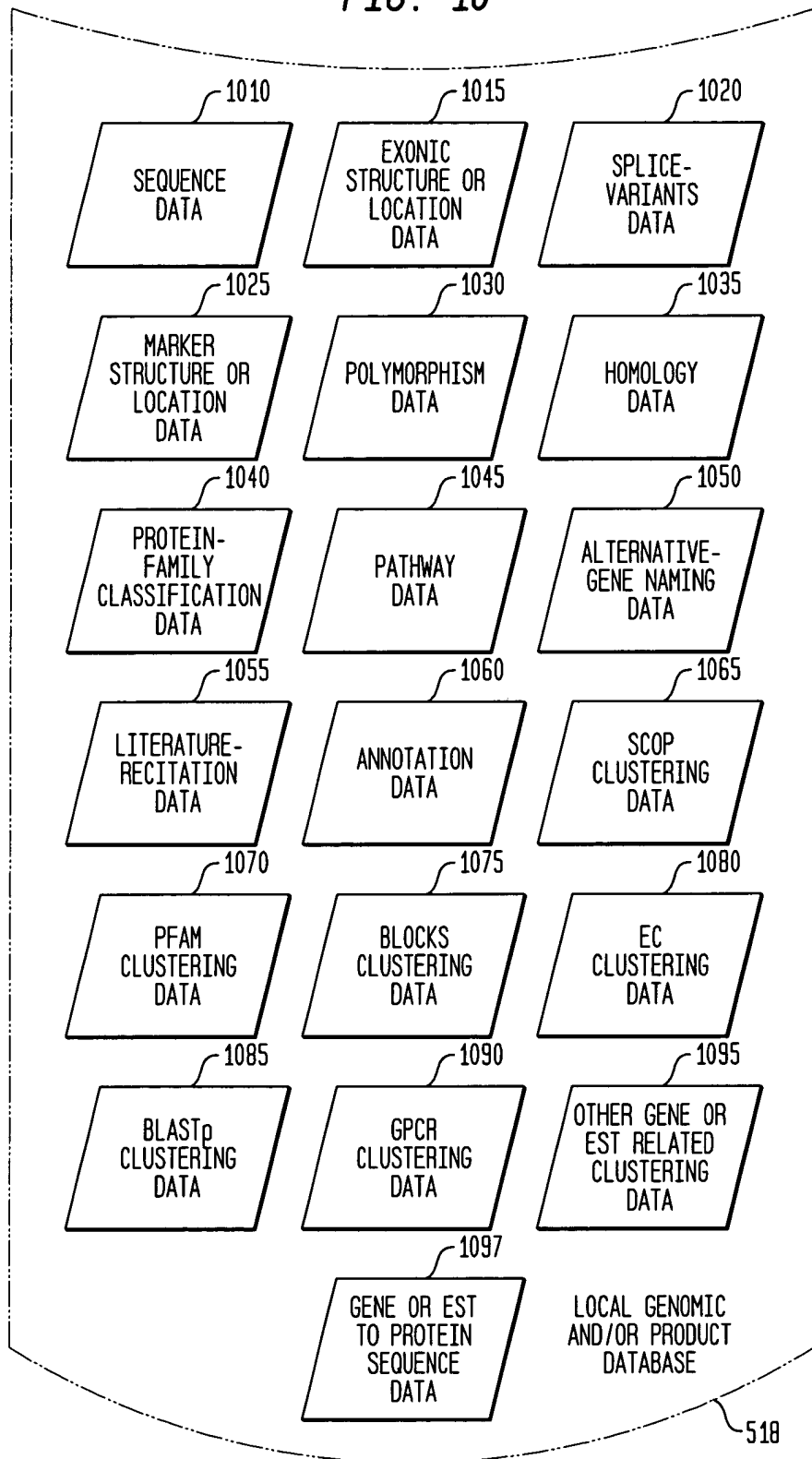


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FIG. 9

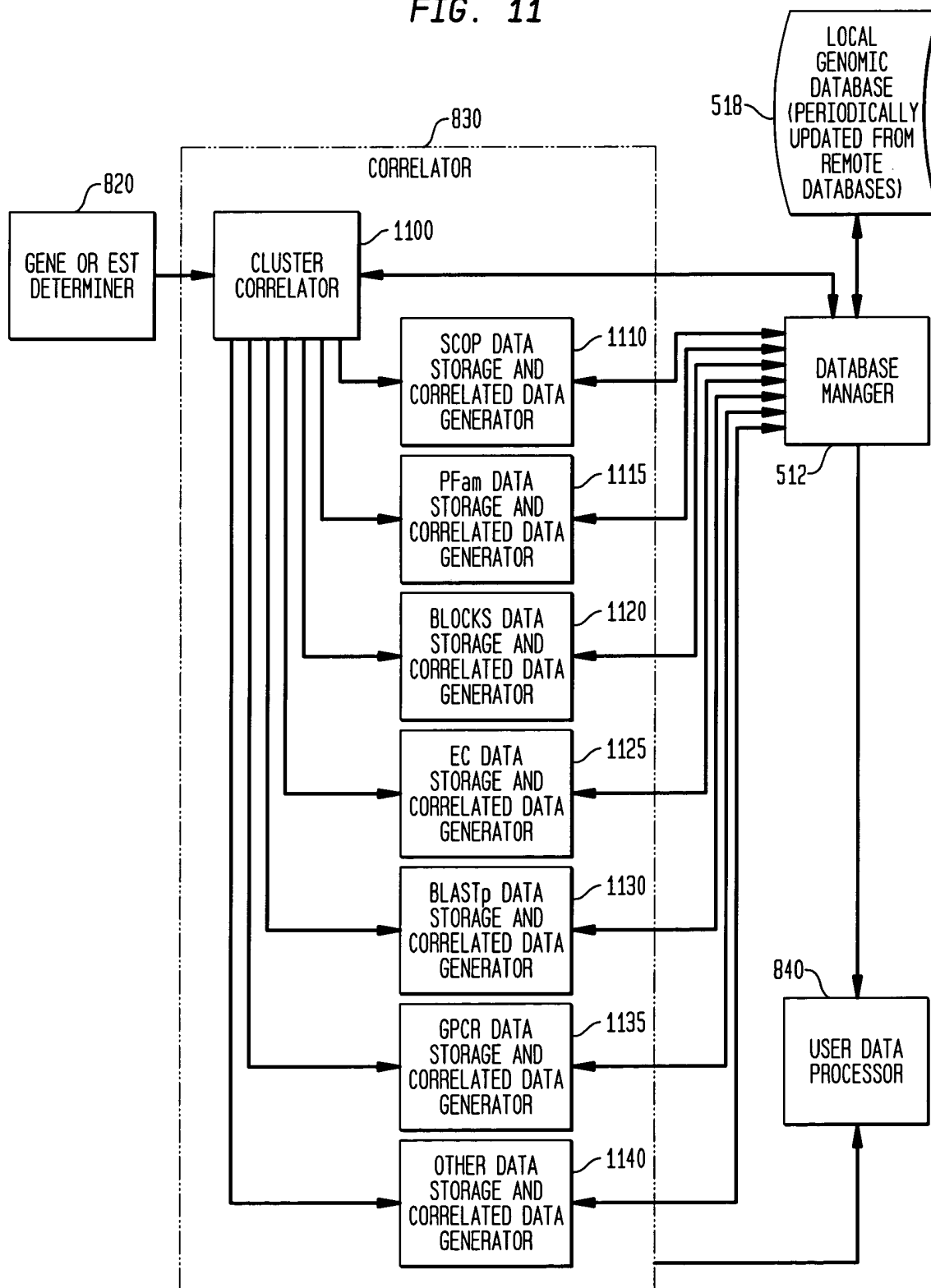


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FIG. 10



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FIG. 11





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FIG. 12

GUI
1200

PROTEIN
IDENTIFIER
1240

Domains_PFAM_Hs:NP_003828
ID NP_003828
SEARCH_METHOD hmmpfam
HIT_NAME FBPase WUSTL
HIT_DESC Fructose-1-6-bisphosphatase
OVERALL_EXPECT 1.5e-179 LOG10-179
SIMSPAN Query 12 _ 335 Target 1 _ 342; EXPECT 1.5e-179 LOG10 -
179;
ALIGNMENT
FBPase: domain 1 of 1, from 12 to 335: score 609.9, E = 1.5e-179
*->iTLtrfileeqgedalaKNEatgeltldlssLalaakeiartIarag
+TLtr ++e+ g+ a+ tgelt+ll+s +a k+i+++++ag
NP_003828 12 LTLTRYVMEK-GRQAK----GTGELTQLLSMLTAIKAISSAVRKAG
53

LanllGlagatNsqGDeQKkLDViaddifinAlkasgvvavlaSEEedel
La+l+G+ag++N++GDe+KkLDV+++ ++in+L++s ++vl+SEE++++
NP_003828 54 LAHLYGIAGSVNVTGDEVKKLDVLSNSLVINMLQSSYSTCVLVSEENKDA
103

//

CLUSTER METHOD
IDENTIFIER
1210

RETURNED FAMILY
DATA
1220

1230
RETURNED ALIGNMENT
DATA